

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/591,447ADATE: 12/10/97  
TIME: 15:13:45

INPUT SET: S22013.raw

This Raw Listing contains the General  
Information Section and up to the first 50 pages.

## SEQUENCE LISTING

- 1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: QUENTIN-MILLET al., Marie-Jose et  
6  
7 (ii) TITLE OF INVENTION: TBP2 FRAGMENTS OF THE TRANSFERRIN  
8 RECEPTOR OF NEISSERIA MENINGITIDIS  
9  
10 (iii) NUMBER OF SEQUENCES: 44  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: LARSON AND TAYLOR  
14 (B) STREET: 1199 NORTH FAIRFAX STREET  
15 (C) CITY: ALEXANDRIA  
16 (D) STATE: VIRGINIA  
17 (E) COUNTRY: USA  
18 (F) ZIP: 22314  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: Floppy disk  
22 (B) COMPUTER: IBM PC compatible  
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER: US 08/591,447  
28 (B) FILING DATE: 29-JAN-1996  
29 (C) CLASSIFICATION:  
30  
31 (viii) ATTORNEY/AGENT INFORMATION:  
32 (A) NAME: SARRO, THOMAS P  
33 (B) REGISTRATION NUMBER: 19,196  
34 (C) REFERENCE/DOCKET NUMBER: XI/P02956  
35  
36 (ix) TELECOMMUNICATION INFORMATION:  
37 (A) TELEPHONE: 703-739-4900  
38 (B) TELEFAX: 703-739-9577  
39  
40  
41 (2) INFORMATION FOR SEQ ID NO:1:  
42  
43 (i) SEQUENCE CHARACTERISTICS:  
44 (A) LENGTH: 2230 base pairs  
45 (B) TYPE: nucleic acid  
46 (C) STRANDEDNESS: single

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47 (D) TOPOLOGY: linear  
48  
49 (ii) MOLECULE TYPE: DNA (genomic)  
50  
51 (vi) ORIGINAL SOURCE:  
52 (A) ORGANISM: Neisseria meningitidis  
53 (B) STRAIN: IM2169  
54  
55 (ix) FEATURE:  
56 (A) NAME/KEY: sig\_peptide  
57 (B) LOCATION: 60..119  
58  
59 (ix) FEATURE:  
60 (A) NAME/KEY: mat\_peptide  
61 (B) LOCATION: 120..2192  
62  
63 (ix) FEATURE:  
64 (A) NAME/KEY: CDS  
65 (B) LOCATION: 60..2192  
66  
67 (ix) FEATURE:  
68 (A) NAME/KEY: misc\_feature  
69 (B) LOCATION: 120..1154  
70  
71 (ix) FEATURE:  
72 (A) NAME/KEY: misc\_feature  
73 (B) LOCATION: 1155..1748  
74  
75 (ix) FEATURE:  
76 (A) NAME/KEY: misc\_feature  
77 (B) LOCATION: 1749..2192  
78  
79 (ix) FEATURE:  
80 (A) NAME/KEY: misc\_binding  
81 (B) LOCATION: 237..1169  
82  
83  
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
85  
86 ATTTGTTAAA AATAAATAAA ATAATAATCC TTATCATTCT TTAATTGAAT TGGGTTTAT 59  
87  
88 ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 107  
89 Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
90 -20 -15 -10 -5  
91  
92 TTG TTG AGT GCC TGT CTG GGC GGC GGC GGC AGT TTC GAT CTT GAT TCT 155  
93 Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser  
94 1 5 10  
95  
96 GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT 203  
97 Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser  
98 15 20 25  
99

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/591,447A

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|     |   |     |
|-----|---|-----|
| 100 | TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG | 251 |
| 101 | Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala |     |
| 102 | 30 35 40  |     |
| 103 |   |     |
| 104 | ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG | 299 |
| 105 | Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu |     |
| 106 | 45 50 55 60   |     |
| 107 |   |     |
| 108 | GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA | 347 |
| 109 | Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys |     |
| 110 | 65 70 75  |     |
| 111 |   |     |
| 112 | CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA | 395 |
| 113 | Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu |     |
| 114 | 80 85 90  |     |
| 115 |   |     |
| 116 | ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA | 443 |
| 117 | Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser |     |
| 118 | 95 100 105  |     |
| 119 |   |     |
| 120 | AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT | 491 |
| 121 | Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn |     |
| 122 | 110 115 120   |     |
| 123 |   |     |
| 124 | CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT | 539 |
| 125 | Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe |     |
| 126 | 125 130 135 140   |     |
| 127 |   |     |
| 128 | TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG | 587 |
| 129 | Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys |     |
| 130 | 145 150 155   |     |
| 131 |   |     |
| 132 | TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA | 635 |
| 133 | Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg |     |
| 134 | 160 165 170   |     |
| 135 |   |     |
| 136 | CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT | 683 |
| 137 | Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe |     |
| 138 | 175 180 185   |     |
| 139 |   |     |
| 140 | GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT | 731 |
| 141 | Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro |     |
| 142 | 190 195 200   |     |
| 143 |   |     |
| 144 | TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC | 779 |
| 145 | Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser |     |
| 146 | 205 210 215 220   |     |
| 147 |   |     |
| 148 | GAA GAA TAT TCC AAC AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG | 827 |
| 149 | Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu |     |
| 150 | 225 230 235   |     |
| 151 |   |     |
| 152 | GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AAT AAG AAA | 875 |

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|     |   |      |
|-----|---|------|
| 153 | Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys |      |
| 154 | 240 245 250   |      |
| 155 |   |      |
| 156 | TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AGC CTA AAT AAT AAT ACT | 923  |
| 157 | Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr |      |
| 158 | 255 260 265   |      |
| 159 |   |      |
| 160 | AAT AAT GAC AAA CAT ACC ACC CAA TAC TAC AGC CTT GAT GCA CAA ATA | 971  |
| 161 | Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile |      |
| 162 | 270 275 280   |      |
| 163 |   |      |
| 164 | ACA GGC AAC CGC TTC AAC GGC ACG GCA ACG GCA ACT GAC AAA AAA GAG | 1019 |
| 165 | Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu |      |
| 166 | 285 290 295 300   |      |
| 167 |   |      |
| 168 | AAT GAA ACC AAA CTA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC | 1067 |
| 169 | Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser |      |
| 170 | 305 310 315   |      |
| 171 |   |      |
| 172 | GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT TTC CGC TTT TTG | 1115 |
| 173 | Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu |      |
| 174 | 320 325 330   |      |
| 175 |   |      |
| 176 | AGC GAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG AAA ACC AAA GAC | 1163 |
| 177 | Ser Asp Asp Gln Lys Val Ala Val Gly Ser Ala Lys Thr Lys Asp     |      |
| 178 | 335 340 345   |      |
| 179 |   |      |
| 180 | AAA CTG GAA AAT GGC GCG GCG GCT TCA GGC AGC ACA GGT GCG GCA GCA | 1211 |
| 181 | Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala |      |
| 182 | 350 355 360   |      |
| 183 |   |      |
| 184 | TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG | 1259 |
| 185 | Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr |      |
| 186 | 365 370 375 380   |      |
| 187 |   |      |
| 188 | GTT TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT | 1307 |
| 189 | Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn |      |
| 190 | 385 390 395   |      |
| 191 |   |      |
| 192 | CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG | 1355 |
| 193 | Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met |      |
| 194 | 400 405 410   |      |
| 195 |   |      |
| 196 | ATT CCG CTC CTG CCC AAG GAT TCC GAA AGC GGG AAC ACT CAG GCA GAT | 1403 |
| 197 | Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp |      |
| 198 | 415 420 425   |      |
| 199 |   |      |
| 200 | AAA GGT AAA AAC GGC GGA ACA GAA TTT ACC CGC AAA TTT GAA CAC ACG | 1451 |
| 201 | Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr |      |
| 202 | 430 435 440   |      |
| 203 |   |      |
| 204 | CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG | 1499 |
| 205 | Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly |      |

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|     | 445   |     | 450 |  | 455 |  | 460 |      |
|-----|---|-----|-----|--|-----|--|-----|------|
| 206 |   |     |     |  |     |  |     |      |
| 207 |   |     |     |  |     |  |     |      |
| 208 | GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA |     |     |  |     |  |     | 1547 |
| 209 | Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys |     |     |  |     |  |     |      |
| 210 |   | 465 |     |  | 470 |  | 475 |      |
| 211 |   |     |     |  |     |  |     |      |
| 212 | ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC |     |     |  |     |  |     | 1595 |
| 213 | Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr |     |     |  |     |  |     |      |
| 214 |   | 480 |     |  | 485 |  | 490 |      |
| 215 |   |     |     |  |     |  |     |      |
| 216 | GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA |     |     |  |     |  |     | 1643 |
| 217 | Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly |     |     |  |     |  |     |      |
| 218 |   | 495 |     |  | 500 |  | 505 |      |
| 219 |   |     |     |  |     |  |     |      |
| 220 | AAC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG |     |     |  |     |  |     | 1691 |
| 221 | Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met |     |     |  |     |  |     |      |
| 222 |   | 510 |     |  | 515 |  | 520 |      |
| 223 |   |     |     |  |     |  |     |      |
| 224 | TTC CTC CAA GGC GAG CGT ACC GAT GAA AAA GAG ATT CCA ACC GAC CAA |     |     |  |     |  |     | 1739 |
| 225 | Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln |     |     |  |     |  |     |      |
| 226 |   | 525 |     |  | 530 |  | 535 | 540  |
| 227 |   |     |     |  |     |  |     |      |
| 228 | AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AAC GGC ACA |     |     |  |     |  |     | 1787 |
| 229 | Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr |     |     |  |     |  |     |      |
| 230 |   | 545 |     |  | 550 |  | 555 |      |
| 231 |   |     |     |  |     |  |     |      |
| 232 | AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGG GCG GAA |     |     |  |     |  |     | 1835 |
| 233 | Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu |     |     |  |     |  |     |      |
| 234 |   | 560 |     |  | 565 |  | 570 |      |
| 235 |   |     |     |  |     |  |     |      |
| 236 | TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACC GGC AAG TTA ACC GCT |     |     |  |     |  |     | 1883 |
| 237 | Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala |     |     |  |     |  |     |      |
| 238 |   | 575 |     |  | 580 |  | 585 |      |
| 239 |   |     |     |  |     |  |     |      |
| 240 | GAA AAC AGG CAG GCG CAA ACC TTT ACC ATT GAG GGA ATG ATT CAG GGC |     |     |  |     |  |     | 1931 |
| 241 | Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly |     |     |  |     |  |     |      |
| 242 |   | 590 |     |  | 595 |  | 600 |      |
| 243 |   |     |     |  |     |  |     |      |
| 244 | AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT GAT CTC |     |     |  |     |  |     | 1979 |
| 245 | Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu |     |     |  |     |  |     |      |
| 246 |   | 605 |     |  | 610 |  | 615 | 620  |
| 247 |   |     |     |  |     |  |     |      |
| 248 | GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC |     |     |  |     |  |     | 2027 |
| 249 | Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala |     |     |  |     |  |     |      |
| 250 |   | 625 |     |  | 630 |  | 635 |      |
| 251 |   |     |     |  |     |  |     |      |
| 252 | AAG GTA AAG GGC GGT TTT TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA |     |     |  |     |  |     | 2075 |
| 253 | Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly |     |     |  |     |  |     |      |
| 254 |   | 640 |     |  | 645 |  | 650 |      |
| 255 |   |     |     |  |     |  |     |      |
| 256 | TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG GAA AAG GCA ACA GCT ACA |     |     |  |     |  |     | 2123 |
| 257 | Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr |     |     |  |     |  |     |      |
| 258 |   | 655 |     |  | 660 |  | 665 |      |

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**SEQUENCE VERIFICATION REPORT**  
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Original Text